

0590  
12/11

# 6

OIPE

## RAW SEQUENCE LISTING

DATE: 12/06/2001

PATENT APPLICATION: US/09/866,582

TIME: 10:51:36

Input Set : A:\SEQUENCE LISTING.TXT

Output Set: N:\CRF3\12062001\I866582.raw

P.S

ENTERED

4 <110> APPLICANT: Witman, George B.  
5 Pazour, Gregory J.  
6 Rosenbaum, Joel L.  
7 Cole, Douglas G.  
9 <120> TITLE OF INVENTION: INTRAFLLAGELLAR TRANSPORT  
11 <130> FILE REFERENCE: 07917-145001  
13 <140> CURRENT APPLICATION NUMBER: US 09/866,582  
14 <141> CURRENT FILING DATE: 2001-05-24  
16 <150> PRIOR APPLICATION NUMBER: US 60/206,923  
17 <151> PRIOR FILING DATE: 2000-05-24  
19 <160> NUMBER OF SEQ ID NOS: 50  
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 877  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Chlamydomonas reinhardtii  
28 <220> FEATURE:  
29 <221> NAME/KEY: CDS  
30 <222> LOCATION: (114)...(518)  
32 <400> SEQUENCE: 1

33	caccgctgcc gctgaacaga aagtctgcgc agactcgtct tcttgccaag ttcttgccaa	60
34	aaccagcagg cctagaggtt gccttaacct aaatatacaa aacacagagc atc atg	116
35		Met
36		1
38	gac gcg gta gat aga gga gtc tac ttt gac gag gac ttt cat gtc cgc	164
39	Asp Ala Val Asp Arg Gly Val Tyr Phe Asp Glu Asp Phe His Val Arg	
40	5 10 15	
42	att ctt gat gtt gac aag tac aat gct tca aag tcg ctc cag gac aac	212
43	Ile Leu Asp Val Asp Lys Tyr Asn Ala Ser Lys Ser Leu Gln Asp Asn	
44	20 25 30	
46	aca aat gtg ttc att aac aac atc caa aat atg caa ggc ctc gtg gac	260
47	Thr Asn Val Phe Ile Asn Asn Ile Gln Asn Met Gln Gly Leu Val Asp	
48	35 40 45	
50	aag tac gtg tcc gcc atc gac cag cag gtc gag cgg cta gaa gct gaa	308
51	Lys Tyr Val Ser Ala Ile Asp Gln Gln Val Glu Arg Leu Glu Ala Glu	
52	50 55 60 65	
54	aag ctg aag gcc att ggc ctg cgg aac cgg gtg gct gcg ctg agc gag	356
55	Lys Leu Lys Ala Ile Gly Leu Arg Asn Arg Val Ala Ala Leu Ser Glu	
56	70 75 80	
58	gag cgg aaa cgt aaa caa aag gag cag gag cgc atg cta gcg gag aag	404
59	Glu Arg Lys Arg Lys Gln Lys Glu Gln Arg Met Leu Ala Glu Lys	
60	85 90 95	
62	cag gag gag ctt gag agg ctc caa atg gag gag cag tcg ctg atc aag	452
63	Gln Glu Glu Leu Glu Arg Leu Gln Met Glu Glu Gln Ser Leu Ile Lys	
64	100 105 110	
66	gtg aag ggc gag cag gag ctc atg att cag aag ctg tcg gac agc agc	500
67	Val Lys Gly Glu Gln Glu Leu Met Ile Gln Lys Leu Ser Asp Ser Ser	

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68      115      120      125
70 agc ggg gcg gca tac gtg taaacggtgt tcggacgtca tgcgtgcaaa      548
71 Ser Gly Ala Ala Tyr Val
72 130      135
74 ggtagttttgc tctgtgaggg ttggctgagg cggcggaggc tgctattgag gctgcagcat      608
75 gcggtctggt ggcagatgta cataacggta tggggtggtg gcgacagaac gaaacggcga      668
76 ggggtgcgcaa atgtcgtgca gaagcgacgc tacagcatcc atggtacgta gaggttact      728
77 ggggtgtcagt gcgtcgtccg cactgggga cacacttgca gcgaggagcg ccattgtttg      788
78 gcccacggat tgcgtcaagg acttgaacgg cgccagtga ggcggggaat ggaatgtaaa      848
79 caaacgactc gaaaaaaaaa aaaaaaaaaa      877
81 <210> SEQ ID NO: 2
82 <211> LENGTH: 135
83 <212> TYPE: PRT
84 <213> ORGANISM: Chlamydomonas reinhardtii
86 <400> SEQUENCE: 2
87 Met Asp Ala Val Asp Arg Gly Val Tyr Phe Asp Glu Asp Phe His Val
88 1      5      10      15
89 Arg Ile Leu Asp Val Asp Lys Tyr Asn Ala Ser Lys Ser Leu Gln Asp
90      20      25      30
91 Asn Thr Asn Val Phe Ile Asn Asn Ile Gln Asn Met Gln Gly Leu Val
92      35      40      45
93 Asp Lys Tyr Val Ser Ala Ile Asp Gln Gln Val Glu Arg Leu Glu Ala
94      50      55      60
95 Glu Lys Leu Lys Ala Ile Gly Leu Arg Asn Arg Val Ala Ala Leu Ser
96 65      70      75      80
97 Glu Glu Arg Lys Arg Lys Gln Lys Glu Gln Glu Arg Met Leu Ala Glu
98      85      90      95
99 Lys Gln Glu Glu Leu Glu Arg Leu Gln Met Glu Glu Gln Ser Leu Ile
100      100      105      110
101 Lys Val Lys Gly Glu Gln Glu Leu Met Ile Gln Lys Leu Ser Asp Ser
102      115      120      125
103 Ser Ser Gly Ala Ala Tyr Val
104      130      135
106 <210> SEQ ID NO: 3
107 <211> LENGTH: 615
108 <212> TYPE: DNA
109 <213> ORGANISM: Chlamydomonas reinhardtii
111 <220> FEATURE:
112 <221> NAME/KEY: CDS
113 <222> LOCATION: (1)...(612)
115 <400> SEQUENCE: 3
116 atg gtg aag aaa gaa gtg aag ccc atc gat atc acc gca acg cta aga      48
117 Met Val Lys Lys Glu Val Lys Pro Ile Asp Ile Thr Ala Thr Leu Arg
118 1      5      10      15
120 tgc aaa gta gca gta gtc ggc gaa gcg act gtc ggc aag agc gcg ctc      96
121 Cys Lys Val Ala Val Val Gly Glu Ala Thr Val Gly Lys Ser Ala Leu
122      20      25      30
124 atc tct atg ttc acg agt aaa ggc agc aag ttt cta aag gac tat gcg      144
125 Ile Ser Met Phe Thr Ser Lys Gly Ser Lys Phe Leu Lys Asp Tyr Ala

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126          35          40          45
128 atg acg agt ggg gtg gag gtg gtg gta gcc ccg gtg acc att ccg gac      192
129 Met Thr Ser Gly Val Glu Val Val Val Ala Pro Val Thr Ile Pro Asp
130          50          55          60
132 acg acg gtc tgc gtg gag ctc ttt ctg ctg gac acg gcg ggg agc gac      240
133 Thr Thr Val Ser Val Glu Leu Phe Leu Leu Asp Thr Ala Gly Ser Asp
134 65          70          75          80
136 ctg tac aag gag cag ata tgc cag tac tgg aac ggc gta tac tac gcc      288
137 Leu Tyr Lys Glu Gln Ile Ser Gln Tyr Trp Asn Gly Val Tyr Tyr Ala
138          85          90          95
140 att ctc gtg ttc gat gtg agc tct atg gag tcc ttc gag tgc tgc aag      336
141 Ile Leu Val Phe Asp Val Ser Ser Met Glu Ser Phe Glu Ser Cys Lys
142          100          105          110
144 gcg tgg ttt gag ctg ctc aaa tgc gcg cgt ccc gac cgc gag cgg ccg      384
145 Ala Trp Phe Glu Leu Leu Lys Ser Ala Arg Pro Asp Arg Glu Arg Pro
146          115          120          125
148 ctg cgc gcc gtg ctg gtg gcg aac aag acg gac ctt ccg ccg cag cgg      432
149 Leu Arg Ala Val Leu Val Ala Asn Lys Thr Asp Leu Pro Pro Gln Arg
150          130          135          140
152 cac cag gtg cgg ctg gac atg gcg cag gac tgg gcc acc acc aac acc      480
153 His Gln Val Arg Leu Asp Met Ala Gln Asp Trp Ala Thr Thr Asn Thr
154 145          150          155          160
156 ctc gac ttc ttc gac gtg tcc gcg aac ccg ccc ggc aag gac gcg gat      528
157 Leu Asp Phe Phe Asp Val Ser Ala Asn Pro Pro Gly Lys Asp Ala Asp
158          165          170          175
160 gcg ccg ttc ctg tcc atc gcc acc acc ttc tac cgc aac tac gag gac      576
161 Ala Pro Phe Leu Ser Ile Ala Thr Thr Phe Tyr Arg Asn Tyr Glu Asp
162          180          185          190
164 aag gtg gcg gcc ttc cag gac gct tgc cgc aac tac tga      615
165 Lys Val Ala Ala Phe Gln Asp Ala Cys Arg Asn Tyr
166          195          200
168 <210> SEQ ID NO: 4
169 <211> LENGTH: 204
170 <212> TYPE: PRT
171 <213> ORGANISM: Chlamydomonas reinhardtii
173 <400> SEQUENCE: 4
174 Met Val Lys Lys Glu Val Lys Pro Ile Asp Ile Thr Ala Thr Leu Arg
175 1          5          10          15
176 Cys Lys Val Ala Val Val Gly Glu Ala Thr Val Gly Lys Ser Ala Leu
177          20          25          30
178 Ile Ser Met Phe Thr Ser Lys Gly Ser Lys Phe Leu Lys Asp Tyr Ala
179          35          40          45
180 Met Thr Ser Gly Val Glu Val Val Val Ala Pro Val Thr Ile Pro Asp
181          50          55          60
182 Thr Thr Val Ser Val Glu Leu Phe Leu Leu Asp Thr Ala Gly Ser Asp
183 65          70          75          80
184 Leu Tyr Lys Glu Gln Ile Ser Gln Tyr Trp Asn Gly Val Tyr Tyr Ala
185          85          90          95
186 Ile Leu Val Phe Asp Val Ser Ser Met Glu Ser Phe Glu Ser Cys Lys

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```

187          100          105          110
188 Ala Trp Phe Glu Leu Leu Lys Ser Ala Arg Pro Asp Arg Glu Arg Pro
189          115          120          125
190 Leu Arg Ala Val Leu Val Ala Asn Lys Thr Asp Leu Pro Pro Gln Arg
191          130          135          140
192 His Gln Val Arg Leu Asp Met Ala Gln Asp Trp Ala Thr Thr Asn Thr
193 145          150          155          160
194 Leu Asp Phe Phe Asp Val Ser Ala Asn Pro Pro Gly Lys Asp Ala Asp
195          165          170          175
196 Ala Pro Phe Leu Ser Ile Ala Thr Thr Phe Tyr Arg Asn Tyr Glu Asp
197          180          185          190
198 Lys Val Ala Ala Phe Gln Asp Ala Cys Arg Asn Tyr
199          195          200
201 <210> SEQ ID NO: 5
202 <211> LENGTH: 1035
203 <212> TYPE: DNA
204 <213> ORGANISM: Chlamydomonas reinhardtii
206 <220> FEATURE:
207 <221> NAME/KEY: CDS
208 <222> LOCATION: (1)...(1032)
210 <400> SEQUENCE: 5
211 atg gat gac tct atg gac tac cct gac cgc gac ggg gac gac ctg gac      48
212 Met Asp Asp Ser Met Asp Tyr Pro Asp Arg Asp Gly Asp Asp Leu Asp
213 1          5          10          15
215 cag ttc cag ggc acc gcg cgc tcg cag gtc gtg cag aac cag ccg cac      96
216 Gln Phe Gln Gly Thr Ala Arg Ser Gln Val Val Gln Asn Gln Pro His
217          20          25          30
219 gac gag gag gtg aac ctg agt gag tcg gag agc ttc gcg gga gcg gat      144
220 Asp Glu Glu Val Asn Leu Ser Glu Ser Glu Ser Phe Ala Gly Ala Asp
221          35          40          45
223 gag cct cca gct gcg cct aga gat gcg tcg ctc ata gag tca cac gac      192
224 Glu Pro Pro Ala Ala Pro Arg Asp Ala Ser Leu Ile Glu Ser His Asp
225          50          55          60
229 atg gac gag ggg cca gct gct cca gcg cgg aca ctc tca cca acg ggc      240
230 Met Asp Glu Gly Pro Ala Ala Pro Ala Arg Thr Leu Ser Pro Thr Gly
231 65          70          75          80
233 tat gag gct gga aag cac gca cct ggc ggc atc gcc aac tcg gac gag      288
234 Tyr Glu Ala Gly Lys His Ala Pro Gly Gly Ile Ala Asn Ser Asp Glu
235          85          90          95
237 gca ccg ccg ggt gct tac aac gca cag gag tac aag cac ctg aac gtg      336
238 Ala Pro Pro Gly Ala Tyr Asn Ala Gln Glu Tyr Lys His Leu Asn Val
239          100          105          110
241 ggc gag gac gtg cgc gag ctg ttc tcc tac atc ggc cgc tac aag ccg      384
242 Gly Glu Asp Val Arg Glu Leu Phe Ser Tyr Ile Gly Arg Tyr Lys Pro
243          115          120          125
245 cag acg gtg gag ctg gac acg cgc atc aag ccc ttc atc cct gac tac      432
246 Gln Thr Val Glu Leu Asp Thr Arg Ile Lys Pro Phe Ile Pro Asp Tyr
247          130          135          140
249 atc ccc gcg gtg ggc ggc atc gac gag ttc atc aag gtg ccg cga ccc      480

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```

250 Ile Pro Ala Val Gly Gly Ile Asp Glu Phe Ile Lys Val Pro Arg Pro
251 145 150 155 160
253 gac acc aag ccc gac tac ctg ggg ctc aag gtt ctg gac gag ccg gcc 528
254 Asp Thr Lys Pro Asp Tyr Leu Gly Leu Lys Val Leu Asp Glu Pro Ala
255 165 170 175
257 gcc aag cag tcg gac ccc acg gtg ctg acg ctg cag ctg cgg cag ctg 576
258 Ala Lys Gln Ser Asp Pro Thr Val Leu Thr Leu Gln Leu Arg Gln Leu
259 180 185 190
261 tcc aag gag gcg ccg ggc gcc aag gcc gac atg gtg ggg cgg ctg gag 624
262 Ser Lys Glu Ala Pro Gly Ala Lys Ala Asp Met Val Gly Arg Leu Glu
263 195 200 205
265 cac acc gac gag aac aag gcc aag aag atc cag cag tgg atc gcc tcc 672
266 His Thr Asp Glu Asn Lys Ala Lys Lys Ile Gln Gln Trp Ile Ala Ser
267 210 215 220
269 atc aac gac atc cac aag gcc aag ccg gcc gcc acc gtc aac tac agc 720
270 Ile Asn Asp Ile His Lys Ala Lys Pro Ala Ala Thr Val Asn Tyr Ser
271 225 230 235 240
273 aag cgc atg cca gag atc gag gcg ctg atg cag gag tgg ccg ccg gag 768
274 Lys Arg Met Pro Glu Ile Glu Ala Leu Met Gln Glu Trp Pro Pro Glu
275 245 250 255
277 gtg gag acc ttc ctc aag acc atg cac atg ccg tcc ggc gat gtg gag 816
278 Val Glu Thr Phe Leu Lys Thr Met His Met Pro Ser Gly Asp Val Glu
279 260 265 270
281 ctg gac atc aag acc tac gcc ccg ctg gtg tgc acg ctg ctg gac att 864
282 Leu Asp Ile Lys Thr Tyr Ala Arg Leu Val Cys Thr Leu Leu Asp Ile
283 275 280 285
286 ccc gtg tac gac gac ccc gtg gag agc ctg cac gtg ctg ttc aca ctg 912
287 Pro Val Tyr Asp Asp Pro Val Glu Ser Leu His Val Leu Phe Thr Leu
288 290 295 300
290 tac ctg gag ttc aag aac aac ccc atc ttc agg cag cac atg gag atg 960
291 Tyr Leu Glu Phe Lys Asn Asn Pro Ile Phe Arg Gln His Met Glu Met
292 305 310 315 320
294 gag aac aag ctg gac ggc atg tcg ggc ggc ggc ggc atg atg ggc 1008
295 Glu Asn Lys Leu Asp Gly Met Ser Gly Gly Gly Gly Met Met Gly
296 325 330 335
298 ggc ggc gcg gat gtg ctg ggc ttg tga 1035
299 Gly Gly Ala Asp Val Leu Gly Leu
300 340
302 <210> SEQ ID NO: 6
303 <211> LENGTH: 344
304 <212> TYPE: PRT
305 <213> ORGANISM: Chlamydomonas reinhardtii
307 <400> SEQUENCE: 6
308 Met Asp Asp Ser Met Asp Tyr Pro Asp Arg Asp Gly Asp Asp Leu Asp
309 1 5 10 15
310 Gln Phe Gln Gly Thr Ala Arg Ser Gln Val Val Gln Asn Gln Pro His
311 20 25 30
312 Asp Glu Glu Val Asn Leu Ser Glu Ser Glu Ser Phe Ala Gly Ala Asp
313 35 40 45

```

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\SEQUENCE LISTING.TXT

Output Set: N:\CRF3\12062001\I866582.raw

L:2212 M:258 W: Mandatory Feature missing, &lt;223&gt; not found for SEQ ID#:21

L:2212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21

L:2328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22

L:2378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24

L:2410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25